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Making Single-Cell Biology Work

New Collaboration Between EMBL-EBI, the Wellcome Trust Sanger Institute and Fluidigm

New Collaboration Between EMBL-EBI, the Wellcome Trust Sanger Institute and Fluidigm Keeps Research and Technology on the Cutting-Edge of Single-Cell Genomics

SOUTH SAN FRANCISCO, Calif., HINXTON, U.K., Dec. 17, 2014 – A formal collaboration was announced today between the Wellcome Trust Sanger Institute, the European Bioinformatics Institute (EMBL-EBI) and Fluidigm Corporation (NASDAQ:FLDM) to accelerate the development of new methods for the analysis of single-cell genomics data.

The Single Cell Genomics Centre (SCGC) on the Wellcome Trust Genome Campus will work with onsite Fluidigm senior staff to ensure that the centre has early access to the latest equipment, workflows and methods for genomics and proteomics research.

“Because we have early access to the most advanced technology, we can develop new experimental and computational methods that help us understand what is happening in each of our cells, at different points in the cell cycle,” says Dr. Sarah Teichmann of EMBL-EBI and the Sanger Institute. “This is really a new frontier – we hope the work we do will help the technology mature more quickly, so that it can help more people find answers to complex biological questions.”

In addition to technology advancements, the collaboration will make single-cell research more accessible to the greater research community by developing and disseminating new workflows, bioinformatics tools, and data sets.

The collaboration builds on previous work between Fluidigm and founding members of the SCGC. For example, the Teichmann group discovered that immune cells produce steroids to regulate themselves – knowledge based on mRNA-seq data from single cells prepared by Fluidigm technology. Using single-cell gene expression data from Fluidigm’s C1™ Single-Cell Auto Prep system and sequencing technology, John Marioni’s group at EMBL-EBI developed a novel statistical method that shows how single-cell mRNA sequencing can be used to pinpoint true differences between cells in apparently homogeneous samples. Thierry Voet, based at KU Leuven and an associate member of Faculty at the Sanger Institute, uses DNA sequencing at the single-cell level to understand how spontaneous variations in DNA can arise as cells divide.

“Our work with the SCGC is about co-creating a solid foundation for a revolution in biological understanding that will come from single-cell analysis,” said Robert C. Jones, Fluidigm Executive Vice President of Research and Development. “Together, we can build better informatics tools to extract relevant biology from the massive amounts of single-cell RNA expression data that our systems generate. We’ll also find innovative ways to determine the DNA, protein, RNA, and epigenetic state of each cell and to scale the process up to perform across thousands and millions of cells.”
These high-throughput techniques allow researchers to explore cellular heterogeneity in normal development and in disease at the single-cell level, offering a vast improvement over the current practice of investigating millions of cells in bulk. Until now, scientists have been limited in their ability to identify functionally distinct subpopulations of cells and understand their contribution into the development of diseases such as cancer. DNA-seq and RNA-seq techniques, enabled by Fluidigm, are opening up new opportunities to discover and explore the diverse nature of cells at the highest possible resolution.

Notes to Editors:

FLUIDIGM TECHNOLOGY

The Single-Cell Genomics Centre employs Fluidigm’s C1 Single-Cell Auto Prep and Biomark™ HD systems, and has access to Fluidigm’s CyTOF® mass spectrometry technology as well.

PUBLICATIONS:

Mahata B et al. Single-cell RNA sequencing reveals T helper cells synthesizing steroids de novo to contribute to immune homeostasis. Cell Reports 2014 May 22; **7(4)**: 1130-42. (http://europepmc.org/abstract/MED/24813893)

Brennecke P et al. Accounting for technical noise in single-cell RNA-seq experiments. Nature Methods 2013 Nov; **10(11)**:

1093-5. (http://europepmc.org/abstract/MED/24056876)

Voet T et al. Single-cell paired-end genome sequencing reveals structural variation per cell cycle. Nucleic Acids Research. Jul 2013; **41(12)**: 6119–6138. (http://europepmc.org/abstract/MED/23630320)

Use of Forward-Looking Statements

This press release contains forward-looking statements within the meaning of the Private Securities Litigation Reform Act of 1995, including statements relating to the SCGC collaboration, Fluidigm's products, and the field of single-cell biology research. Forward-looking statements are subject to numerous risks and uncertainties that could cause actual results to differ materially from currently anticipated results, including inherent risks relating to research and development activities and emerging markets. Information on these and additional risks affecting Fluidigm's business and operating results are contained in its filings with the Securities and Exchange Commission, including its most recently filed Quarterly Report on Form 10-Q for the quarter ended September 30, 2014. These forward-looking statements speak only as of the date hereof and Fluidigm disclaims any obligation to update these statements except as may be required by law.

About Fluidigm

Fluidigm (NASDAQ:FLDM) develops, manufactures, and markets life science analytical and preparatory systems for growth markets such as single-cell biology and production genomics. We sell to leading academic institutions, clinical laboratories, and pharmaceutical, biotechnology, and agricultural biotechnology companies worldwide. Our systems are based on proprietary microfluidics and multi-parameter mass cytometry technology, and are designed to significantly simplify experimental workflow, increase throughput, and reduce costs, while providing excellent data quality. Fluidigm products are provided for Research Use Only. Not for use in diagnostic procedures.

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